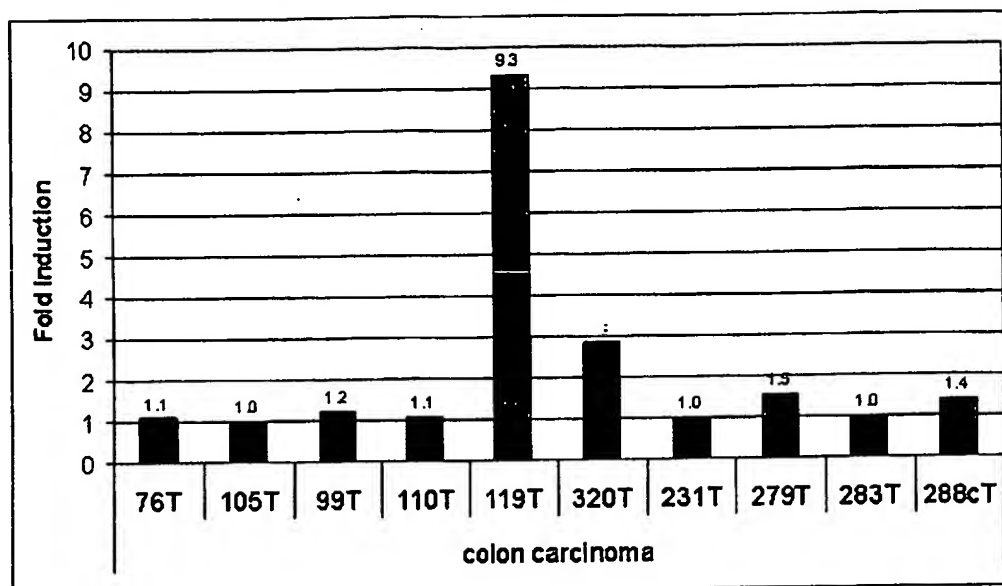
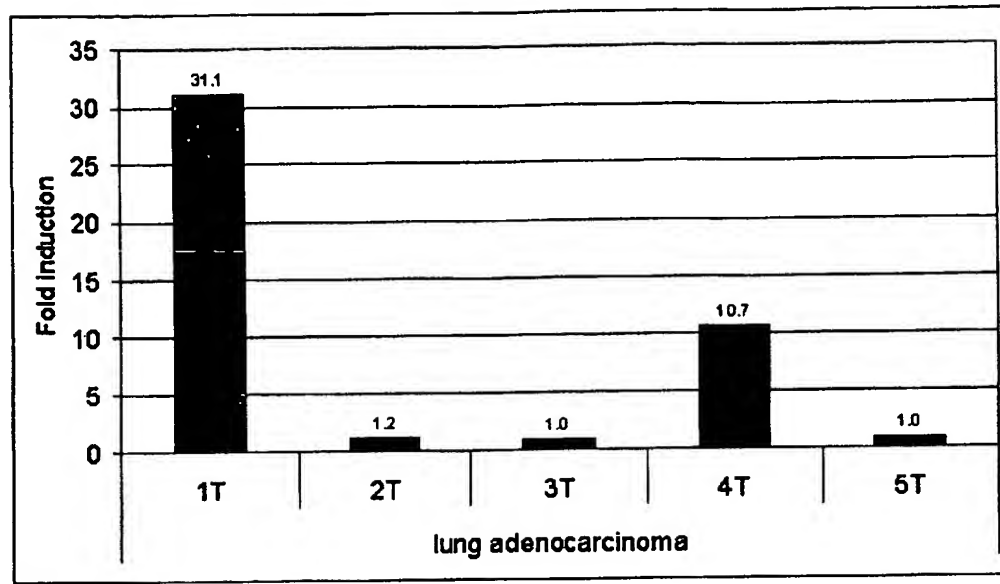


Figure 1:



TKT-L1

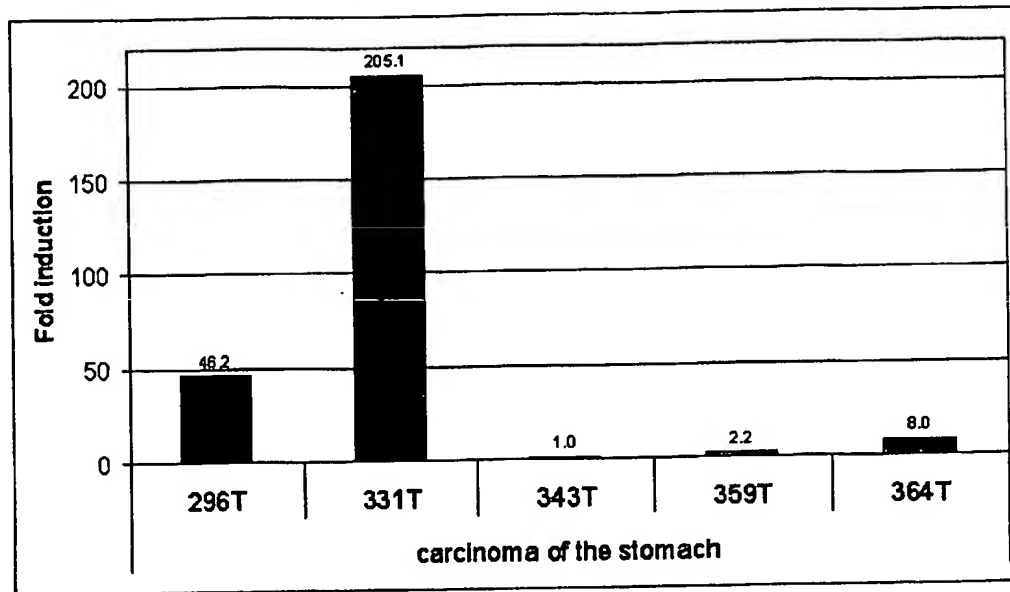
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TKT-L1

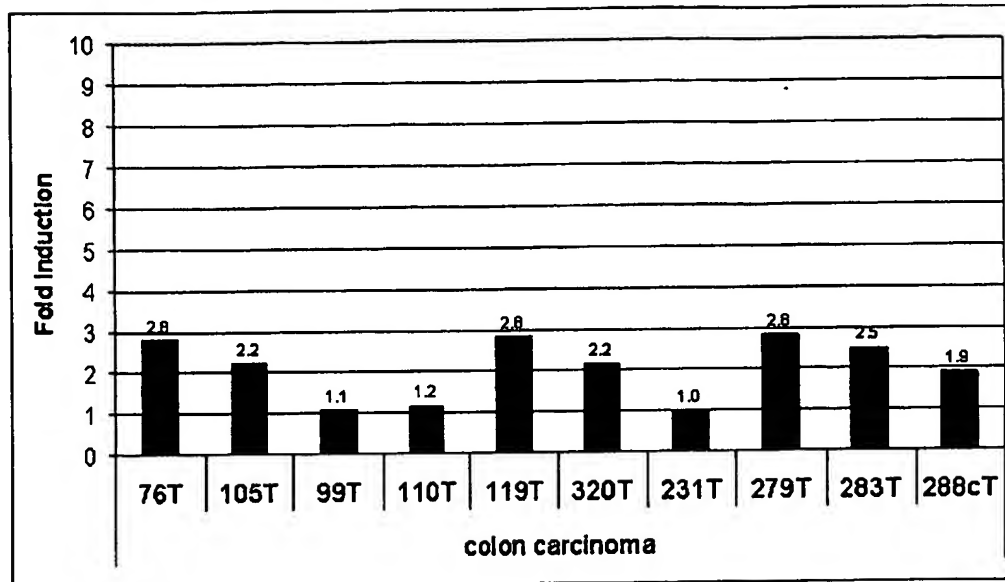
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Figure 3:



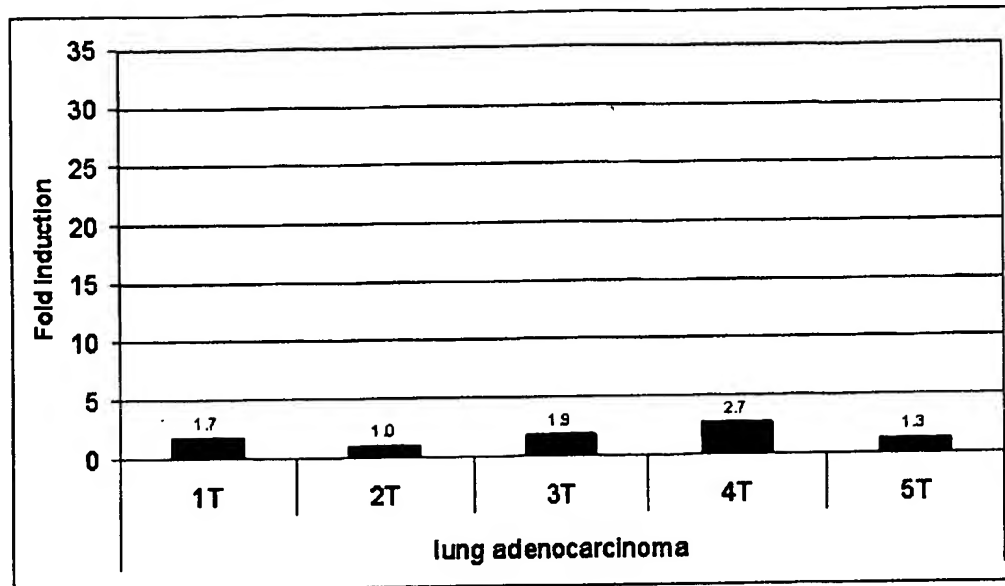
TKT-L1

Figure 4:



TKT

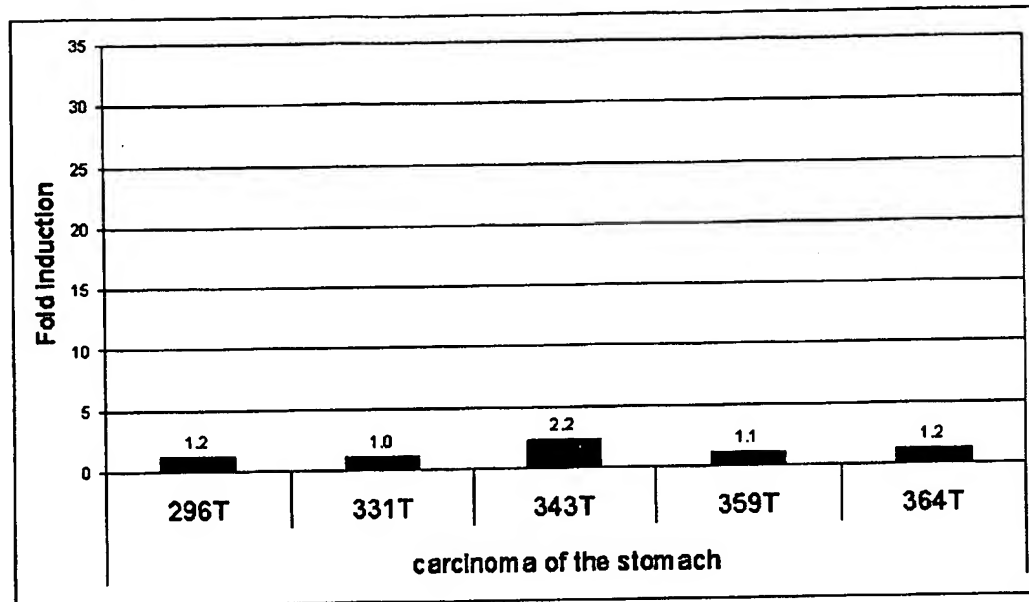
Figure 5:



TKT

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Figure 6



TKT

Fig. 7: DNA and amino acid sequence of TKT-L1

1 GCCATTGCTCTTCAGACGCCGGAGACGTAGGAGTGGGTCTTCAGACTCCAAAGGGGTG  
61 GACTAATGGCGGATGCTGAGGCGAGGGCTGAGTTCCTCGAGGAGGCCAGACCTGACAGGG  
M A D A E A R A E F P E E A R P D R G  
121 GCACCTTGCAGGTGTTGCAAGATATGGCCAGCCGCTTGCGAATCCATTCCATCAGGGCCA  
T L Q V L Q D M A S R L R I H S I R A T  
181 CATGCTCCACGAGCTCCGGCCACCCTACATCATGTAGCAGTTCTTCTGAGATCATGTCTG  
C S T S S G H P T S C S S S S E I M S V  
241 TGCTGTCTTCTACATCATGAGGTACAAGCAGTCAGATCCAGAGAATCCGGACAACGACC  
L F F Y I M R Y K Q S D P E N P D N D R  
301 GATTTGCTCTCGCAAAGAGACTGTGCTTGTGGATGTGGCAACAGGATGGCTCGGACAAG  
F V L A K R L S F V D V A T G W L G Q G  
361 GACTGGGAGTTGCATGTGGAATGGCATATACTGGCAAGTACTTCGACAGGGCCAGCTACC  
L G V A C G M A Y T G K Y F D R A S Y R  
421 GGGTGTCTGCCTCATGAGTGATGGCGAGTCTCAGAAGGCTCTGTCTGGGAGGCAATGG  
V F C L M S D G E S S E G S V W E A M A  
481 CCTTTGCTTCCTACTACAGTCTGGACAATCTTGTGGCAATCTTTGATGTGAACCGCCTGG  
F A S Y Y S L D N L V A I F D V N R L G  
541 GACACAGTGGTGCATTGCCCCCGAGCACTGCATAAACATCTATCAGAGGCGCTGCGAAG  
H S G A L P A E H C I N I Y Q R R C E A  
601 CCTTTGGGTGGAACACTTATGTGGTGGACGGCCGGGACGTGGAGGCACTGTGCCAGGTAT  
F G W N T Y V V D G R D V E A L C Q V F  
661 TCTGGCAGGCTTCTCAGGTGAAGCACAAGCCCACTGCTGTGGTGGCCAAGACCTTCAAGG  
W Q A S Q V K H K P T A V V A K T F K G  
721 GCCGGGGCACCCCAAGTATTGAGGATGCAGAAAGTTGGCATGCAAAGCCAATGCCGAGAG  
R G T P S I E D A E S W H A K P M P R E  
781 AAAGAGCAGATGCCATTATCAAATTAATTGAGAGCCAGATACAGACCAGCAGGAATCTTG  
R A D A I I K L I E S Q I Q T S R N L D  
841 ACCCACAGCCCCCATTGAGGACTCACCTGAAGTCAACATCACAGATGTAAGGATGACCT  
P Q P P I E D S P E V N I T D V R M T S  
901 CTCCACCTGATTACAGAGTTGGTGACAAGATAGCTACTCGGAAAGCATGCGGTCTGGCTC  
P P D Y R V G D K I A T R K A C G L A L  
961 TGGCTAAGCTGGGCTACGCCGAACAACAGAGTCGTTGTGCTGGATGGTGACACCAGGTA  
A K L G Y A N N R V V V L D G D T R Y S  
1021 CTACTTTCTCTGAGATATTCAACAAGGAGTACCCTGAGCGCTTCATCGAGTGCCTTATGG  
T F S E I F N K E Y P E R F I E C F M A  
1081 CTGAACAAAACATGGTGAGCGTGGCTCTGGGCTGTGCCTCCCGTGGACGGACCATTGCTT  
E Q N M V S V A L G C A S R G R T I A F  
1141 TTGCTAGCACCTTTGCTGCCCTTCTGACTCGAGCATTTGATCACATCCGATAGGAGGCC  
A S T F A A F L T R A F D H I R I G G L

1201 TCGCTGAGAGCAACATCAACATTATTGGTTCCCACTGTGGGGTATCTGTTGGTGACGATG  
A E S N I N I I G S H C G V S V G D D G

1261 GTGCTTCCCAGATGGCCCTGGAGGATATAGCCATGTTCCGAACCATTCCCAAGTGCACGA  
A S Q M A L E D I A M F R T I P K C T I

1321 TCTTCTACCCAACTGATGCCGTCTCCACGGAGCATGCTGTTGCTCTGGCAGCCAATGCCA  
F Y P T D A V S T E H A V A L A A N A K

1381 AGGGGATGTGCTTCATTCCGACCACCCGACCAGAACTATGGTTATTTACACCCCAACAG  
G M C F I R T T R P E T M V I Y T P Q E

1441 AACGCTTTGAGATCGGACAGGCCAAGGTCCTCCGCCACTGTGTCAGTGACAAGGTCACAG  
R F E I G Q A K V L R H C V S D K V T V

1501 TTATTGGAGCTGGAATTACTGTGTATGAAGCCTTAGCAGCTGCTGATGAGCTTTGAAAC  
I G A G I T V Y E A L A A A D E L S K Q

1561 AAGATATTTTATCCGTGTCATCGACCTGTTTACCATTAAACCTCTGGATGTCGCCACCA  
D I F I R V I D L F T I K P L D V A T I

1621 TCGTCTCCAGTGCAAAAGCCACAGAGGGCCGGATCATTACAGTGGAGGATCACTACCCGC  
V S S A K A T E G R I I T V E D H Y P Q

1681 AAGGTGGCATCGGGGAAGCTGTCTGCGCAGCCGTCTCCATGGATCCTGACATTCAGGTTG  
G G I G E A V C A A V S M D P D I Q V H

1741 ATTCGCTGGCAGTGTGGGAGTGCCCCAGAGTGGGAAGTCCGAGGAATTGCTGGATATGT  
S L A V S G V P Q S G K S E E L L D M Y

1801 ATGGAATTAGTGCCAGACATATCATAGTGGCCGTGAAATGCATGTTGCTGAACTAAAATA  
G I S A R H I I V A V K C M L L N \*

1861 GCTGTTAGCCTTGGTCTTTTGGCCTCTTTACCCTGTGTTTATGTTTGTTCAAAACCATC

1921 ATTTAAATCTCTACTGTCACATTTTGTTCCTTAAAAGCAAAGCCAGCTAACACCTTCATT

1981 CATCCCTAGTTCGGAAATTCAAGCTAACTACTTACCCTTTAAACTGTCACTGCATATGCA

2041 AGTACCGCTCTAATTTTGGATCATTAAGGGAGTTACACAACCTTTTAAGTGAAAAAAT

2101 AGGTAACAAAACAACACCTGATAGTAAGTTTCTGATAAGACTATAGATAAGTGGTAGA

2161 GGTAATCAATCTTCCGAAGTGTTCCTTCGTGAATAACTGGTAGAGGTAATAGTTTTTT

2221 CAATGTATTTCTTCATGAGTAAAGAAAATGTGGATTGAAGTATAGATTCCAGTAGCCTA

2281 GTTTCACAGCACGATAACACCATGACGCCTACTGCTGTTCCACCTTGGGATTCTGTGT

2341 GCTGCCATCCACCTGCAGCTGCCCTGGAATTCCTTCGCTGTTTGCCTTCATCTCCCTC

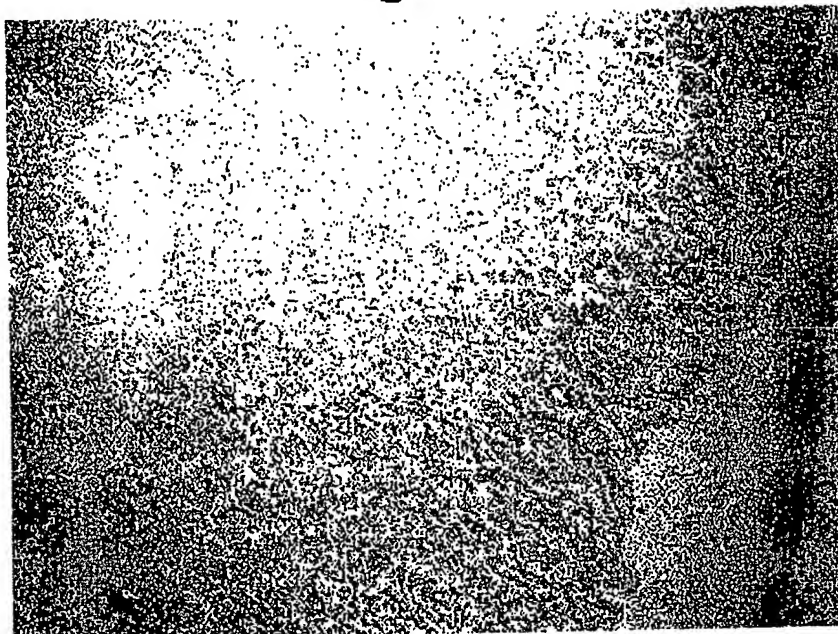
2401 CACGTTTGAGAGGCTGTGAGGCAGCAGCGAAAGCTGTAGGATGTCCTGTGCTGCTGTGT

2461 GATGAGAGCCTCCACACTGTACTGTTCAAGTCAATGTTAATAAAGCATTTCAAACCAAA

2521 AAAAAAAAAA



Fig. 8



A

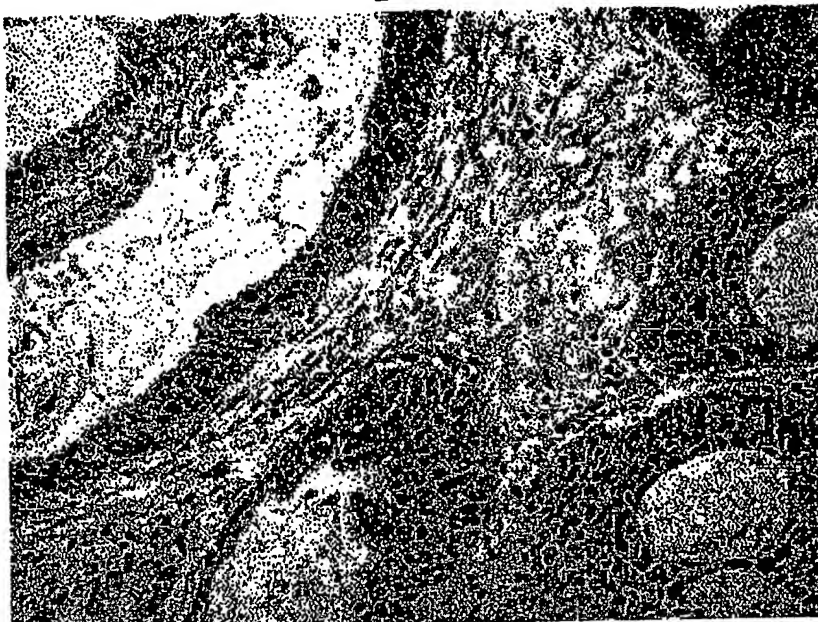
1666



B

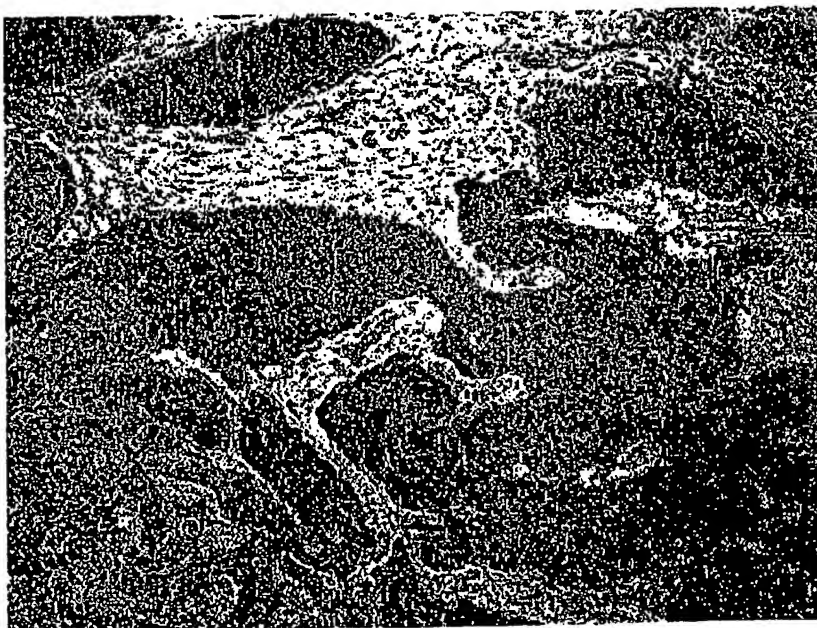
1666

Fig.9



A

1682



B

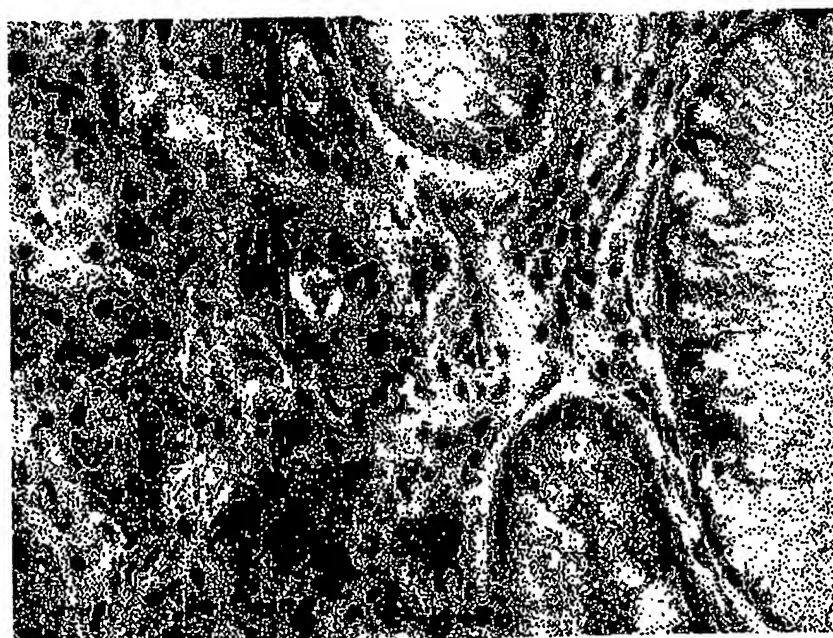
1697

Fig.10



A

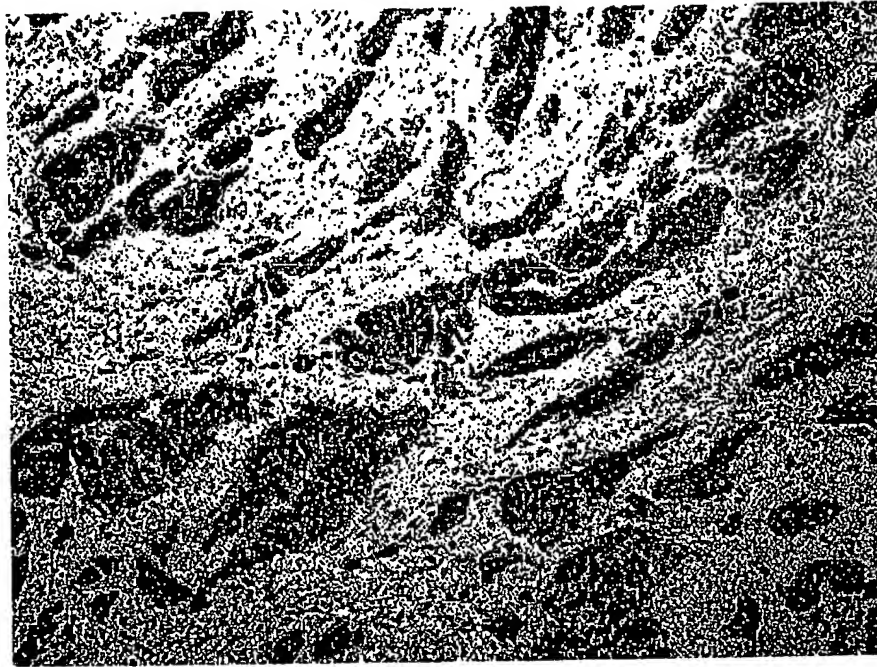
1699



B

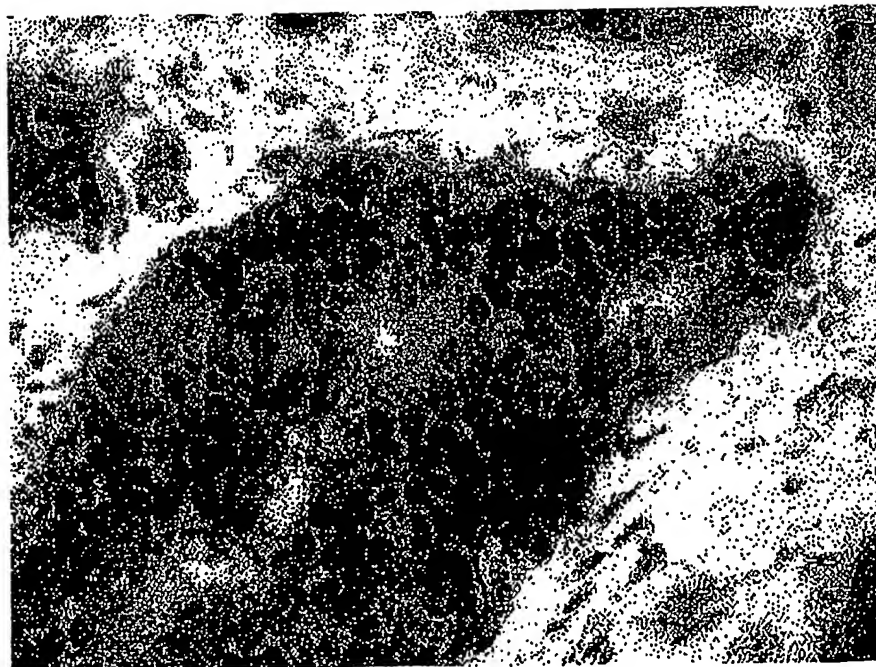
1699

Fig.11



A

1698



B

1698

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